

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study. [For final submission](#): please carefully check your responses for accuracy; you will not be able to make changes later.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- | n/a | Confirmed |
|-------------------------------------|---|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted <i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

- | | |
|-----------------|---|
| Data collection | <input type="text" value="No software was used to collect data."/> |
| Data analysis | <input type="text" value="All code used to analyze and produce the results can be found in the referenced main github repository (https://github.com/almaan/stereoscope), it has also been deposited at Zenodo (doi : 10.5281/zenodo.3951884). Code for the method DWLS was accessed at https://github.com/dtsoucas/DWLS (with a slightly modified version, due to bugs) uploaded to the main (Stereoscope) github repository. Code for deconvSeq was accessed at https://github.com/rostedu1/deconvSeq."/> |

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Links to publicly available datasets:

Spatial Data:

- Human Developmental Heart (ST1K): <https://www.spatialresearch.org/resources-published-datasets/doi-10-1016-j-cell-2019-11-025/>
- Mouse Hippocampus (Visium) : https://support.10xgenomics.com/spatial-gene-expression/datasets/1.0.0/V1_Adult_Mouse_Brain
- Mouse Hippocampus (Slide-seq) : https://singlecell.broadinstitute.org/single_cell/study/SCP354/slide-seq-study (Puck ID : 180413_7)
- Mouse Cerebellum (Slide-seq) : https://singlecell.broadinstitute.org/single_cell/study/SCP354/slide-seq-study (Puck ID : 180819_11)
- Mouse Hippocampus (ST1K) : <https://github.com/almaan/stereoscope/blob/master/data/mousebrain/mouse-st-data.zip> (password : zNLXkYk3Q9znUseS)

Single Cell data:

- Mouse Hippocampus : https://storage.googleapis.com/linnarsson-lab-loom/l1_hippocampus.loom
- Mouse Cerebellum : https://storage.googleapis.com/linnarsson-lab-loom/l1_cerebellum.loom
- Human Developmental Heart : <https://www.spatialresearch.org/resources-published-datasets/doi-10-1016-j-cell-2019-11-025/>

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

- Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

| | |
|-----------------|--|
| Sample size | Only publicly available data was used in the study. Hence, we did not construct the experimental design and/or decide on the number of individuals by which the data was sampled nor the number of data points collected for each sample. |
| Data exclusions | We did not actively exclude any datasets. The single cell data was at times subsampled, to reduce computational cost, when implemented this was done by randomly sampling cells from each annotated cell type (see Methods). In the array based spatial data (ST1K and Visium), only spots under the tissue were used. All beads with non-zero counts were included in the Slide-seq analysis. |
| Replication | See field "Sample size". We show reproducibility by using data from multiple technical platforms (ST1K, Visium and Slide-seq), as well as replicates for one of these instances (ST1K). |
| Randomization | See field "Sample size". We are not assessing effect size in association to an intervention or similar. Randomization is of no relevancy to our work. |
| Blinding | See field "Randomization". |

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

- | n/a | Involved in the study |
|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern |

Methods

- | n/a | Involved in the study |
|-------------------------------------|---|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |